

**REMARKS**

Entry of the foregoing amendment, and further favorable reconsideration of the subject application in light of the following remarks, pursuant to and consistent with 37 C.F.R. § 1.116, are respectfully requested. The amendment does not present any additional claims; and places the application in better form for an appeal should an appeal become necessary.

As indicated in the Office Action Summary, claims 35-58 and 60-119 were pending in the application. Claims 49-52, 57, 58, 60-63, 76, 77, 83, 84, and 108-119 are under consideration and stand rejected. Claims 35-48, 53-56, 64-75, 78-82 and 85-107 have been withdrawn from consideration.

By the present amendment, claims 35-48, 53-56, 64-75, 78-82 and 85-107 have been canceled without prejudice or disclaimer of the subject matter described therein. Additionally, claims 49-51, 57, 58, 61 and 108-111 have been amended. Support for the amendment to claims 49-51 can be found throughout the specification, with particular reference to the first full paragraph on page 7 and the final paragraph of page 8. Further support for the amendment to claims 57, 58 and 61 can be found throughout the specification, with particular reference to the first full paragraph on page 7 and the final paragraph of page 8 and also with reference to pages 4-7 and 18-19.

No new matter is added by way of the present amendment. Any subject matter that may have been canceled by the present amendment is canceled without prejudice or disclaimer. The right to file a continuation or divisional application directed to any canceled subject matter is reserved.

**Claim rejections under 35 USC § 112:**

Claims 49-52, 57, 58, 60-63, 76, 83, 84 and 108-119 have been rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to comply with the written description requirement.

The Office has acknowledged that the specification discloses SEQ ID NO: 1, which meets the written description guidelines. However, the Office has alleged that the claims embrace products containing sequences that do not meet the written description guidelines and methods of using such products.

The rejection is respectfully traversed. The claims as previously presented recited sequences selected from the group consisting of a sequence according to SEQ ID NO 1 with an open reading frame from base pair 211 to base pair 1740, a sequence which is at least 50% homologous with the sequence according to SEQ ID NO 1, and a sequence which hybridizes with the sequence according to SEQ ID NO 1 under stringent conditions, wherein said sequence codes for a plant protein having fucosyl transferase activity; and sections of such sequences.

The Office has acknowledged that sequence according to SEQ ID NO 1 with an open reading frame from base pair 211 to base pair 1740 is adequately described.

The genus of sequences which are at least 50% homologous with the sequence according to SEQ ID NO 1 represents a mathematically defined set of sequences that could be instantly recognized by computer sequence comparison. Further, one skilled in the art would be able to predict which of such sequences would code for a protein having fucosyl transferase activity by reference to SEQ ID NO 1 as a representative species, for example, sequences having silent mutations, having mutations encoding conservative amino acid substitutions, and mutations that do not substantially disturb the conserved sequence

according to SEQ ID NO: 3, which is described beginning at page 6 of the specification. The foregoing notwithstanding, the issue of homologous sequences has been obviated as the recitations of sequences which are at least 50% homologous with the sequence according to SEQ ID NO 1 and code for a plant protein having fucosyl transferase activity have been deleted from claims 49-51.

The genus of sequences which hybridize with the sequence according to SEQ ID NO 1 under stringent conditions and codes for a plant protein having fucosyl transferase activity is clearly a sufficiently described genus. The training materials of the Office for the application of the Written Description guidelines have explained that such a genus is adequately described in a situation such as in the present application. *See, e.g.,* Example 9 of the *Revised Interim Written Description Guidelines Training Materials* that is currently published by the Office at <http://www.uspto.gov/web/offices/pac/writtendesc.pdf>.

Now turning to the genus analysis, a person of skill in the art would not expect substantial variation among species encompassed within the scope of the claims because the highly stringent hybridization conditions set forth in the claim yield structurally similar DNAs. Thus, a representative number of species is disclosed, since highly stringent hybridization conditions in combination with the coding function of DNA and the level of skill and knowledge in the art are adequate to determine that applicant was in possession of the claimed invention.

It is noted that stringent hybridization conditions are defined in the specification of the present application at page 5. The requirement of stringent hybridization to a specific sequence is sufficient description of the recited sequences. A person of ordinary skill in the art would not expect substantial variation among species encompassed within the scope of this recitation such that a person skilled in the art would be able to recognize sequences within the genus and would have appreciated that the inventors were in possession of the recited genus.

Thus, claims 49-51, 57, 58, 61 and 108-111 have been amended without agreeing with or acquiescing to the alleged basis of the rejection. For example, the recitation of sequences which are at least 50% homologous with the sequence according to SEQ ID NO 1 and that the selected sequence codes for a plant protein having fucosyl transferase activity are deleted from claims 49-51.

Claims 49-50 are directed to a vector for expressing antisense DNA. Claim 51 is directed to a DNA molecule encoding a ribozyme. As such, one skilled in the art would recognize that it is not necessary that the sequence(s), or partial sequence(s), contained in these constructs actually encode a protein having fucosyl transferase activity. Rather, the antisense sequence need only hybridize with the target sequence.

Claims 49-51 as amended recite sequences, or part sequences, according to SEQ ID NO:1 or that hybridize under stringent conditions to a sequence according to SEQ ID NO:1. The recited genus of sequences are adequately described, as acknowledged by the Office with respect to SEQ ID NO:1 itself, and because SEQ ID NO:1 discloses a sufficient representative of the genus of sequences that will hybridize to SEQ ID NO:1 under stringent conditions, for essentially the reasons explained in Example 9 (Hybridization) of the *Revised Interim Written Description Guidelines Training Materials* that is currently published by the Office at <http://www.uspto.gov/web/offices/pac/writtendesc.pdf>.

Claims 57-58 and 61 are directed to methods of preparing recombinant hosts comprising a vector expressing an antisense molecule or of preparing a recombinant host comprising a homologous recombination. Claims 57-58 and 61 have been amended to better describe the claimed subject matter. Claims 57-58 and 61 now recite a step of identifying a DNA sequence in a host that codes for a protein having fucosyl transferase activity using SEQ ID NO:1 as a reference, such that the identified sequence corresponds to a part of SEQ

ID NO:1 or bears sufficient similarity to be more than 50% homologous or to hybridize under stringent conditions. The host is prepared by inserting a DNA molecule derived from the identified sequence.

The identification step is fully described and can be performed on any of the recited hosts by routine experimentation. At pages 18-19, the specification describes how to identify fucosyl transferase coding sequences in hosts using sequences from SEQ ID NO:1. At page 6, the specification teaches that the conserved sequence of SEQ ID NO:3 is particularly useful for sequence recognition. Of course, the identification of a sequence need not comprise a screening step. Sequences may also be identified from the knowledge of the skilled practitioner by sequence comparison methods using SEQ ID NO:1, for example, in mung bean, or where genome sequencing data is available or by reference to experience whenever the method is repeated on a host of a given type.

Thus, a person of ordinary skill would recognize that the claimed method can be practiced on any of the recited hosts, and that the inventors were in possession of the method as claimed at the time the application was filed.

For at least the foregoing reasons, the claims as currently presented meet that written description and thus withdrawal of the rejection under 35 U.S.C. § 112, first paragraph, is respectfully requested.

### **CONCLUSION**

In view of the foregoing, further and favorable action in the form of a Notice of Allowance is believed to be next in order. Such action is earnestly solicited.

In the event that there are any questions relating to this application, it would be appreciated if the Examiner would telephone the undersigned concerning such questions so that prosecution of this application may be expedited.

The Director is hereby authorized to charge any appropriate fees that may be required by this paper, and to credit any overpayment, to Deposit Account No. 02-4800.

Respectfully submitted,

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Date: September 6, 2005

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